WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising the nucleotide sequence that encodes a protein having the following amino acid sequence:

Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-
Leu-Ser-Val-Ile-Met-Glu-Glu-Met-Lys-Leu-Val-Asp-Ser-Lys-His-Gly-
Gln-Leu-Ile-Lys-Asn-Phe-Thr-Ile-Leu-Gln-Gly-Pro-Pro-Gly-Pro-Arg-
Gly-Pro-Arg-Gly-Asp-Arg-Gly-Ser-Gln-Gly-Pro-Pro-Gly-Pro-Thr-Gly-
Asn-Lys-Gly-Gln-Lys-Gly-Glu-Lys-Gly-Glu-Pro-Gly-Pro-Pro-Gly-Pro-
Ala-Gly-Glu-Arg-Gly-Pro-Ile-Gly-Pro-Ala-Gly-Pro-Pro-Gly-Glu-Arg-
Gly-Gly-Lys-Gly-Ser-Lys-Gly-Ser-Gln-Gly-Pro-Lys-Gly-Ser-Arg-Gly-
Ser-Pro-Gly-Lys-Pro-Gly-Pro-Gln-Gly-Pro-Ser-Gly-Asp-Pro-Gly-Pro-
Pro-Gly-Pro-Pro-Gly-Lys-Glu-Gly-Leu-Pro-Gly-Pro-Gln-Gly-Pro-Pro-
Gly-Phe-Gln-Gly-Leu-Gln-Gly-Thr-Val-Gly-Glu-Pro-Gly-Val-Pro-Gly-
Pro-Arg-Gly-Leu-Pro-Gly-Leu-Pro-Gly-Val-Pro-Gly-Met-Pro-Gly-Pro-
Lys-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Pro-Ser-Gly-Ala-Val-Val-Pro-Leu-
Ala-Leu-Gln-Asn-Glu-Pro-Thr-Pro-Ala-Pro-Glu-Asp-Asn-Gly-Cys-Pro-
Pro-His-Trp-Lys-Asn-Phe-Thr-Asp-Lys-Cys-Tyr-Tyr-Phe-Ser-Val-Glu-
Lys-Glu-Ile-Phe-Glu-Asp-Ala-Lys-Leu-Phe-Cys-Glu-Asp-Lys-Ser-Ser-
His-Leu-Val-Phe-Ile-Asn-Thr-Arg-Glu-Glu-Gln-Gln-Trp-Ile-Lys-Lys-
Gln-Met-Val-Gly-Arg-Glu-Ser-His-Trp-Ile-Gly-Leu-Thr-Asp-Ser-Glu-
Arg-Glu-Asn-Glu-Trp-Lys-Trp-Leu-Asp-Gly-Thr-Ser-Pro-Asp-Tyr-Lys-
Asn-Trp-Lys-Ala-Gly-Gln-Pro-Asp-Asn-Trp-Gly-His-Gly-His-Gly-Pro-
Gly-Glu-Asp-Cys-Ala-Gly-Leu-Ile-Tyr-Ala-Gly-Gln-Trp-Asn-Asp-Phe-
Gln-Cys-Glu-Asp-Val-Asn-Asn-Phe-Ile-Cys-Glu-Lys-Asp-Arg-Glu-Thr-
Val-Leu-Ser-Ser-Ala-Leu (SEQ ID NO:2, 206-547).

2. An isolated polynucleotide comprising the nucleotide sequence that

encodes a protein having the following amino acid sequence:

Met-Lys-Leu-Val-Asp-Ser-Lys-His-Gly-Gln-Leu-Ile-Lys-Asn-Phe-Thr-Ile-Leu-Gln-Gly-Pro-Pro-Gly-Pro-Arg-Gly-Pro-Arg-Gly-Asp-Arg-Gly-Ser-Gln-Gly-Pro-Pro-Gly-Pro-Thr-Gly-Asn-Lys-Gly-Gln-Lys-Gly-Glu-Lys-Gly-Glu-Pro-Gly-Pro-Pro-Gly-Pro-Ala-Gly-Glu-Arg-Gly-Pro-Ile-Gly-Pro-Ala-Gly-Pro-Pro-Gly-Glu-Arg-Gly-Gly-Lys-Gly-Ser-Lys-Gly-Ser-Gln-Gly-Pro-Lys-Gly-Ser-Arg-Gly-Ser-Pro-Gly-Lys-Pro-Gly-Pro-Gln-Gly-Pro-Ser-Gly-Asp-Pro-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Lys-Glu-Gly-Leu-Pro-Gly-Pro-Gln-Gly-Pro-Pro-Gly-Phe-Gln-Gly-Leu-Gln-Gly-Thr-Val-Gly-Glu-Pro-Gly-Val-Pro-Gly-Pro-Arg-Gly-Leu-Pro-Gly-Leu-Pro-Gly-Val-Pro-Gly-Met-Pro-Gly-Pro-Lys-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Pro-Ser-Gly-Ala-Val-Val-Pro-Leu-Ala-Leu-Gln-Asn-Glu-Pro-Thr-Pro-Ala-Pro-Glu-Asp-Asn-Gly-Cys-Pro-Pro-His-Trp-Lys-Asn-Phe-Thr-Asp-Lys-Cys-Tyr-Tyr-Phe-Ser-Val-Glu-Lys-Glu-Ile-Phe-Glu-Asp-Ala-Lys-Leu-Phe-Cys-Glu-Asp-Lys-Ser-Ser-His-Leu-Val-Phe-Ile-Asn-Thr-Arg-Glu-Glu-Gln-Gln-Trp-Ile-Lys-Lys-Gln-Met-Val-Gly-Arg-Glu-Ser-His-Trp-Ile-Gly-Leu-Thr-Asp-Ser-Glu-Arg-Glu-Asn-Glu-Trp-Lys-Trp-Leu-Asp-Gly-Thr-Ser-Pro-Asp-Tyr-Lys-Asn-Trp-Lys-Ala-Gly-Gln-Pro-Asp-Asn-Trp-Gly-His-Gly-His-Gly-Pro-Gly-Glu-Asp-Cys-Ala-Gly-Leu-Ile-Tyr-Ala-Gly-Gln-Trp-Asn-Asp-Phe-Gln-Cys-Glu-Asp-Val-Asn-Asn-Phe-Ile-Cys-Glu-Lys-Asp-Arg-Glu-Thr-Val-Leu-Ser-Ser-Ala-Leu (SEQ ID NO: 2, 229-547).

3. The polynucleotide according to claim 2, wherein said protein further comprises the following amino acid sequence upstream of the first methionine residue (SEQ ID NO:2, 229):

Met-Glu-Glu (SEQ ID NO: 2, 226-228); or

Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 211-228).

4. The polynucleotide according to claim 2, wherein said protein further comprises the following amino acid sequence upstream of the first methionine residue (SEQ ID NO:2, 229):

Met-Glu-Asn-Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 102-228);

Met-Asn-Ser-Gln-Leu-Asn-Ser-Phe-Thr-Gly-Gln-Met-Glu-Asn-Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 91-228);

Met-Asn-Leu-Asn-Asn-Leu-Asn-Leu-Thr-Gln-Val-Gln-Gln-Arg-Asn-Leu-

Ile-Thr-Asn-Leu-Gln-Arg-Ser-Val-Asp-Asp-Thr-Ser-Gln-Ala-Ile-Gln-Arg-Ile-Lys-Asn-Asp-Phe-Gln-Asn-Leu-Gln-Gln-Val-Phe-Leu-Gln-Ala-Lys-Lys-Asp-Thr-Asp-Trp-Leu-Lys-Glu-Lys-Val-Gln-Ser-Leu-Gln-Thr-Leu-Ala-Ala-Asn-Asn-Ser-Ala-Leu-Ala-Lys-Ala-Asn-Asn-Asp-Thr-Leu-Glu-Asp-Met-Asn-Ser-Gln-Leu-Asn-Ser-Phe-Thr-Gly-Gln-Met-Glu-Asn-Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 9-228);

or

Met-Tyr-Ser-His-Asn-Val-Val-Ile-Met-Asn-Leu-Asn-Asn-Leu-Asn-Leu-Thr-Gln-Val-Gln-Gln-Arg-Asn-Leu-Ile-Thr-Asn-Leu-Gln-Arg-Ser-Val-Asp-Asp-Thr-Ser-Gln-Ala-Ile-Gln-Arg-Ile-Lys-Asn-Asp-Phe-Gln-Asn-Leu-Gln-Gln-Val-Phe-Leu-Gln-Ala-Lys-Lys-Asp-Thr-Asp-Trp-Leu-Lys-Glu-Lys-Val-Gln-Ser-Leu-Gln-Thr-Leu-Ala-Ala-Asn-Asn-Ser-Ala-Leu-Ala-Lys-Ala-Asn-Asn-Asp-Thr-Leu-Glu-Asp-Met-Asn-Ser-Gln-Leu-Asn-Ser-Phe-Thr-Gly-Gln-Met-Glu-Asn-Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-

Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 1-228).

5. An isolated polynucleotide comprising a nucleotide sequence having the following nucleotide sequence:

atgcaacaag atttgatgag gtcgaggtta gacactgaag tagccaactt atcagtgatt atggaagaaa tgaagctagt agactccaag catggtcagc tcatcaagaa ttttacaata ctacaaggtc caccgggccc caggggtcca agaggtgaca gaggatccca gggacccccc ggcccaactg gcaacaaggg acagaaagga gagaaggggg agcctggacc acctggccct gcgggtgaga gaggcccaat tggaccagct ggtccccccg gagagcgtgg cggcaaagga tctaaaggct cccagggccc caaaggctcc cgtggttccc ctgggaagcc cggccctcag ggccccagtg gggacccagg ccccccgggc ccaccaggca aagagggact ccccggccct cagggccctc ctggcttcca gggacttcag ggcaccgttg gggagcctgg ggtgcctgga cctcggggac tgccaggctt gcctggggta ccaggcatgc caggccccaa gggccccccc ggccctcctg gcccatcagg agcggtggtg ccccctggcc tgcagaatga gccaaccccg gcaccggagg acaatggctg cccgcctcac tggaagaact tcacagacaa atgctactat ttttcagttg agaaagaaat ttttgaggat gcaaagcttt tctgtgaaga caagtcttca catcttgttt tcataaacac tagagaggaa cagcaatgga taaaaaaaca gatggtaggg agagagagcc actggatcgg cctcacagac tcagagcgtg aaaatgaatg gaagtggctg gatgggacat ctccagacta caaaaattgg aaagctggac agccggataa ctggggtcat ggccatgggc caggagaaga ctgtgctggg ttgatttatg ctgggcagtg gaacgatttc caatgtgaag acgtcaataa cttcatttgc gaaaaagaca gggagacagt actgtcatct gcatta (SEQ ID NO: 1, 670-1695).

6. An isolated polynucleotide comprising a nucleotide sequence having

the following nucleotide sequence:

atgaagctag tagactccaa gcatggtcag ctcatcaaga attttacaat actacaaggt
ccaccgggcc ccaggggtcc aagaggtgac agaggatccc agggaccccc tggcccaact
ggcaacaagg gacagaaagg agagaagggg gagcctggac cacctggccc tgcgggtgag
agaggcccaa ttggaccagc tggtcccccc ggagagcgtg gcggcaaagg atctaaaggc
tcccagggcc ccaaaggctc ccgtggttcc cctgggaagc ccggccctca gggccccagt
ggggacccag gccccccggg cccaccaggc aaagagggac tccccggccc tcagggccct
cctggcttcc agggacttca gggcaccgtt ggggagcctg gggtgcctgg acctcgggga
ctgccaggct tgcctggggt accaggcatg ccaggcccca agggcccccc cggccctcct
ggcccatcag gagcggtggt gcccctggcc ctgcagaatg agccaacccc ggcaccggag
gacaatggct gcccgcctca ctggaagaac ttcacagaca aatgctacta tttttcagtt
gagaaagaaa tttttgagga tgcaaagctt ttctgtgaag acaagtcttc acatcttgtt
ttcataaaca ctagagagga acagcaatgg ataaaaaaac agatggtagg gagagagagc
cactggatcg gcctcacaga ctcagagcgt gaaaatgaat ggaagtggct ggatgggaca
tctccagact acaaaaattg gaaagctgga cagcaggata actggggtca tggccatggg
ccaggagaag actgtgctgg gttgatttat gctgggcagt ggaacgattt ccaatgtgaa
gacgtcaata acttcatttg cgaaaaagac agggagacag tactgtcatc tgcatta

(SEQ ID NO: 1, 739-1695).

7. The polynucleotide according to claim 6 further comprises the following nucleotide sequence 5' upstream of said nucleotide sequence:

atggaagaa (SEQ ID NO: 1, 730-738); or

atgaggtcga ggttagacac tgaagtagcc aacttatcag tgattatgga agaa (SEQ ID NO: 1, 685-738).

8. The polynucleotide according to claim 6 further comprises the following

nucleotide sequence 5' upstream of said nucleotide sequence:

atggagaaca tcaccactat ctctcaagcc aacgagcaga acctgaaaga cctgcaggac

ttacacaaag atgcagagaa tagaacagcc atcaagttca accaactgga ggaacgcttc

cagctctttg agacggatat tgtgaacatc attagcaata tcagttacac agcccaccac

ctgcggacgc tgaccagcaa tctaaatgaa gtcaggacca cttgcacaga tacccttacc

aaacacacag atgatctgac ctccttgaat aataccctgg ccaacatccg tttggattct

gtttctctca ggatgcaaca agatttgatg aggtcgaggt tagacactga agtagccaac

ttatcagtga ttatggaaga a (SEQ ID NO: 1, 358-738);

atgaacagcc agctcaactc attcacaggt cagatggaga acatcaccac tatctctcaa

gccaacgagc agaacctgaa agacctgcag gacttacaca aagatgcaga gaatagaaca

gccatcaagt tcaaccaact ggaggaacgc ttccagctct ttgagacgga tattgtgaac

atcattagca atatcagtta cacagcccac cacctgcgga cgctgaccag caatctaaat

gaagtcagga ccacttgcac agataccctt accaaacaca cagatgatct gacctccttg

aataataccc tggccaacat ccgtttggat tctgtttctc tcaggatgca acaagatttg

atgaggtcga ggttagacac tgaagtagcc aacttatcag tgattatgga agaa (SEQ ID NO:

1, 325-738);

atgaacctca acaacctgaa cctgacccag gtgcagcaga ggaacctcat cacgaatctg

cagcggtctg tggatgacac aagccaggct atccagcgaa tcaagaacga ctttcaaaat

ctgcagcagg tttttcttca agccaagaag gacacggatt ggctgaagga gaaagtgcag

agcttgcaga cgctggctgc caacaactct gcgttggcca aagccaacaa cgacaccctg

gaggatatga acagccagct caactcattc acaggtcaga tggagaacat caccactatc

tctcaagcca acgagcagaa cctgaaagac ctgcaggact tacacaaaga tgcagagaat

agaacagcca tcaagttcaa ccaactggag gaacgcttcc agctctttga gacggatatt

gtgaacatca ttagcaatat cagttacaca gcccaccacc tgcggacgct gaccagcaat

ctaaatgaag tcaggaccac ttgcacagat acccttacca aacacacaga tgatctgacc

tccttgaata ataccctggc caacatccgt ttggattctg tttctctcag gatgcaacaa

gatttgatga ggtcgaggtt agacactgaa gtagccaact tatcagtgat tatggaagaa (SEQ I D NO: 1, 79-738);

atgtattctc ataatgtggt catcatgaac ctcaacaacc tgaacctgac ccaggtgcag cagaggaacc tcatcacgaa tctgcagcgg tctgtggatg acacaagcca ggctatccag cgaatcaaga acgactttca aaatctgcag caggtttttc ttcaagccaa gaaggacacg gattggctga aggagaaagt gcagagcttg cagacgctgg ctgccaacaa ctctgcgttg gccaaagcca acaacgacac cctggaggat atgaacagcc agctcaactc attcacaggt cagatggaga acatcaccac tatctctcaa gccaacgagc agaacctgaa agacctgcag gacttacaca aagatgcaga gaatagaaca gccatcaagt tcaaccaact ggaggaacgc ttccagctct ttgagacgga tattgtgaac atcattagca atatcagtta cacagcccac cacctgcgga cgctgaccag caatctaaat gaagtcagga ccacttgcac agataccctt accaaacaca cagatgatct gacctccttg aataataccc tggccaacat ccgtttggat tctgtttctc tcaggatgca acaagatttg atgaggtcga ggttagacac tgaagtagcc aacttatcag tgattatgga agaa (SEQ ID NO:1, 55-738); or

gtcacgaatc tgcagcaaga taccagcgtg ctccagggca atctgcagaa ccaaatgtat tctcataatg tggtcatcat gaacctcaac aacctgaacc tgacccaggt gcagcagagg aacctcatca cgaatctgca gcggtctgtg gatgacacaa gccaggctat ccagcgaatc aagaacgact ttcaaaatct gcagcaggtt tttcttcaag ccaagaagga cacggattgg ctgaaggaga aagtgcagag cttgcagacg ctggctgcca acaactctgc gttggccaaa gccaacaacg acaccctgga ggatatgaac agccagctca actcattcac aggtcagatg gagaacatca ccactatctc tcaagccaac gagcagaacc tgaaagacct gcaggactta cacaaagatg cagagaatag aacagccatc aagttcaacc aactggagga acgcttccag ctctttgaga cggatattgt gaacatcatt agcaatatca gttacacagc ccaccacctg cggacgctga ccagcaatct aaatgaagtc aggaccactt gcacagatac cctcaccaaa cacacagatg atctgacctc cttgaataat accctggcca acatccgttt ggattctgtt tctctcagga tgcaacaaga tttgatgagg tcgaggttag acactgaagt agccaactta

tcagtgatta tggaagaa (SEQ ID NO: 1, 1-738).

9. The polynucleotide according to any one of claims 5 to 8 further co mprises the following nucleotide sequence 3' downstream of said nucleotide sequen ce:

taacggactg tgatgggatc acatgagcaa attttcagct ctcaaaggca aaggacactc ctttctaatt gcatcacctt ctcatcagat tgaaaaaaaa aaaagcactg aaaaccaatt actgaaaaaa aattgacagc tagtgttttt taccatccgt cattacccaa agacttggga actaaaatgt tccccagggt gatatgctga ttttcattgt gcacatggac tgaatcacat agattctcct ccgtcagtaa ccgtgcgatt atacaaatta tgtcttccaa agtatggaac actccaatca gaaaaaggtt atcatcccg (SEQ ID NO: 1, 1696-2024).

10. An isolated polynucleotide encoding a novel collectin, which can hybridize under a stringent condition with a probe that is an amplification product from PCR reaction performed using primers having the following nucleotide sequences:

caatctgatgagaaggtgatg(SEQ ID NO: 4) and

acgaggggctggatgggacat(SEQ ID NO: 5).

11. A polynucleotide which can hybridize under a stringent condition with any one of the polynucleotide according to any one of claims 1 to 10, wherein the protein encoded by said polynucleotide is a novel collectin which comprises: (1) Ca^{2+}-dependent carbohydrate recognition domain (CRD), and (2) collagen-like region.

12. The polynucleotide according to any one of claims 1 to 11, wherein said polynucleotide is cDNA.

13. A novel collectin comprising the amino acid sequence encoded by the polynucleotide according to any one of claims 5 to 12.

14. A novel collectin comprising the amino acid sequence:

Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu-Met-Lys-Leu-Val-Asp-Ser-Lys-His-Gly-Gln-Leu-Ile-Lys-Asn-Phe-Thr-Ile-Leu-Gln-Gly-Pro-Pro-Gly-Pro-Arg-Gly-Pro-Arg-Gly-Asp-Arg-Gly-Ser-Gln-Gly-Pro-Pro-Gly-Pro-Thr-Gly-Asn-Lys-Gly-Gln-Lys-Gly-Glu-Lys-Gly-Glu-Pro-Gly-Pro-Pro-Gly-Pro-Ala-Gly-Glu-Arg-Gly-Pro-Ile-Gly-Pro-Ala-Gly-Pro-Pro-Gly-Glu-Arg-Gly-Gly-Lys-Gly-Ser-Lys-Gly-Ser-Gln-Gly-Pro-Lys-Gly-Ser-Arg-Gly-Ser-Pro-Gly-Lys-Pro-Gly-Pro-Gln-Gly-Pro-Ser-Gly-Asp-Pro-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Lys-Glu-Gly-Leu-Pro-Gly-Pro-Gln-Gly-Pro-Pro-Gly-Phe-Gln-Gly-Leu-Gln-Gly-Thr-Val-Gly-Glu-Pro-Gly-Val-Pro-Gly-Pro-Arg-Gly-Leu-Pro-Gly-Leu-Pro-Gly-Val-Pro-Gly-Met-Pro-Gly-Pro-Lys-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Pro-Ser-Gly-Ala-Val-Val-Pro-Leu-Ala-Leu-Gln-Asn-Glu-Pro-Thr-Pro-Ala-Pro-Glu-Asp-Asn-Gly-Cys-Pro-Pro-His-Trp-Lys-Asn-Phe-Thr-Asp-Lys-Cys-Tyr-Tyr-Phe-Ser-Val-Glu-Lys-Glu-Ile-Phe-Glu-Asp-Ala-Lys-Leu-Phe-Cys-Glu-Asp-Lys-Ser-Ser-His-Leu-Val-Phe-Ile-Asn-Thr-Arg-Glu-Glu-Gln-Gln-Trp-Ile-Lys-Lys-Gln-Met-Val-Gly-Arg-Glu-Ser-His-Trp-Ile-Gly-Leu-Thr-Asp-Ser-Glu-Arg-Glu-Asn-Glu-Trp-Lys-Trp-Leu-Asp-Gly-Thr-Ser-Pro-Asp-Tyr-Lys-Asn-Trp-Lys-Ala-Gly-Gln-Pro-Asp-Asn-Trp-Gly-His-Gly-His-Gly-Pro-Gly-Glu-Asp-Cys-Ala-Gly-Leu-Ile-Tyr-Ala-Gly-Gln-Trp-Asn-Asp-Phe-Gln-Cys-Glu-Asp-Val-Asn-Asn-Phe-Ile-Cys-Glu-Lys-Asp-Arg-Glu-Thr-Val-Leu-Ser-Ser-Ala-Leu (SEQ ID NO: 2, 206-547).

15. A novel collectin comprising the amino acid sequence: Met-Lys-Leu-Val-Asp-Ser-Lys-His-Gly-Gln-Leu-Ile-Lys-Asn-Phe-Thr-Ile-Leu-Gln-Gly-Pro-Pro-Gly-Pro-Arg-Gly-Pro-Arg-Gly-Asp-Arg-Gly-

Ser-Gln-Gly-Pro-Pro-Gly-Pro-Thr-Gly-Asn-Lys-Gly-Gln-Lys-Gly-Glu-Lys-Gly-Glu-Pro-Gly-Pro-Pro-Gly-Pro-Ala-Gly-Glu-Arg-Gly-Pro-Ile-Gly-Pro-Ala-Gly-Pro-Pro-Gly-Glu-Arg-Gly-Gly-Lys-Gly-Ser-Lys-Gly-Ser-Gln-Gly-Pro-Lys-Gly-Ser-Arg-Gly-Ser-Pro-Gly-Lys-Pro-Gly-Pro-Gln-Gly-Pro-Ser-Gly-Asp-Pro-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Lys-Glu-Gly-Leu-Pro-Gly-Pro-Gln-Gly-Pro-Pro-Gly-Phe-Gln-Gly-Leu-Gln-Gly-Thr-Val-Gly-Glu-Pro-Gly-Val-Pro-Gly-Pro-Arg-Gly-Leu-Pro-Gly-Leu-Pro-Gly-Val-Pro-Gly-Met-Pro-Gly-Pro-Lys-Gly-Pro-Pro-Gly-Pro-Pro-Gly-Pro-Ser-Gly-Ala-Val-Val-Pro-Leu-Ala-Leu-Gln-Asn-Glu-Pro-Thr-Pro-Ala-Pro-Glu-Asp-Asn-Gly-Cys-Pro-Pro-His-Trp-Lys-Asn-Phe-Thr-Asp-Lys-Cys-Tyr-Tyr-Phe-Ser-Val-Glu-Lys-Glu-Ile-Phe-Glu-Asp-Ala-Lys-Leu-Phe-Cys-Glu-Asp-Lys-Ser-Ser-His-Leu-Val-Phe-Ile-Asn-Thr-Arg-Glu-Glu-Gln-Gln-Trp-Ile-Lys-Lys-Gln-Met-Val-Gly-Arg-Glu-Ser-His-Trp-Ile-Gly-Leu-Thr-Asp-Ser-Glu-Arg-Glu-Asn-Glu-Trp-Lys-Trp-Leu-Asp-Gly-Thr-Ser-Pro-Asp-Tyr-Lys-Asn-Trp-Lys-Ala-Gly-Gln-Pro-Asp-Asn-Trp-Gly-His-Gly-His-Gly-Pro-Gly-Glu-Asp-Cys-Ala-Gly-Leu-Ile-Tyr-Ala-Gly-Gln-Trp-Asn-Asp-Phe-Gln-Cys-Glu-Asp-Val-Asn-Asn-Phe-Ile-Cys-Glu-Lys-Asp-Arg-Glu-Thr-Val-Leu-Ser-Ser-Ala-Leu (SEQ ID NO: 2, 229-547).

16. The novel collectin according to claim 15, wherein said novel collectin further comprises the following amino acid sequence upstream of the first methionine residue (SEQ ID NO: 2, 229):

Met-Glu-Glu (SEQ ID NO: 2, 226-228); or

Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 211-228).

17. The novel collectin according to claim 15, wherein said novel collectin further comprises the following amino acid sequence upstream of the first methionine residue (SEQ ID NO: 2, 229):

Met-Glu-Asn-Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 102-228);

Met-Asn-Ser-Gln-Leu-Asn-Ser-Phe-Thr-Gly-Gln-Met-Glu-Asn-Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 91-228);

Met-Asn-Leu-Asn-Asn-Leu-Asn-Leu-Thr-Gln-Val-Gln-Gln-Arg-Asn-Leu-Ile-Thr-Asn-Leu-Gln-Arg-Ser-Val-Asp-Asp-Thr-Ser-Gln-Ala-Ile-Gln-Arg-Ile-Lys-Asn-Asp-Phe-Gln-Asn-Leu-Gln-Gln-Val-Phe-Leu-Gln-Ala-Lys-Lys-Asp-Thr-Asp-Trp-Leu-Lys-Glu-Lys-Val-Gln-Ser-Leu-Gln-Thr-Leu-Ala-Ala-Asn-Asn-Ser-Ala-Leu-Ala-Lys-Ala-Asn-Asn-Asp-Thr-Leu-Glu-Asp-Met-Asn-Ser-Gln-Leu-Asn-Ser-Phe-Thr-Gly-Gln-Met-Glu-Asn-

Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 9-228); or

Met-Tyr-Ser-His-Asn-Val-Val-Ile-Met-Asn-Leu-Asn-Asn-Leu-Asn-Leu-Thr-Gln-Val-Gln-Gln-Arg-Asn-Leu-Ile-Thr-Asn-Leu-Gln-Arg-Ser-Val-Asp-Asp-Thr-Ser-Gln-Ala-Ile-Gln-Arg-Ile-Lys-Asn-Asp-Phe-Gln-Asn-Leu-Gln-Gln-Val-Phe-Leu-Gln-Ala-Lys-Lys-Asp-Thr-Asp-Trp-Leu-Lys-Glu-Lys-Val-Gln-Ser-Leu-Gln-Thr-Leu-Ala-Ala-Asn-Asn-Ser-Ala-Leu-Ala-Lys-Ala-Asn-Asn-Asp-Thr-Leu-Glu-Asp-Met-Asn-Ser-Gln-Leu-Asn-Ser-Phe-Thr-Gly-Gln-Met-Glu-Asn-Ile-Thr-Thr-Ile-Ser-Gln-Ala-Asn-Glu-Gln-Asn-Leu-Lys-Asp-Leu-Gln-Asp-Leu-His-Lys-Asp-Ala-Glu-Asn-Arg-Thr-Ala-Ile-Lys-Phe-Asn-Gln-Leu-Glu-Glu-Arg-Phe-Gln-Leu-Phe-Glu-Thr-Asp-Ile-Val-Asn-Ile-Ile-Ser-Asn-Ile-Ser-Tyr-Thr-Ala-His-His-Leu-Arg-Thr-Leu-Thr-Ser-Asn-Leu-Asn-Glu-Val-Arg-Thr-Thr-Cys-Thr-Asp-Thr-Leu-Thr-Lys-His-Thr-Asp-Asp-Leu-Thr-Ser-Leu-Asn-Asn-Thr-Leu-Ala-Asn-Ile-Arg-Leu-Asp-Ser-Val-Ser-Leu-Arg-Met-Gln-Gln-Asp-Leu-Met-Arg-Ser-Arg-Leu-Asp-Thr-Glu-Val-Ala-Asn-Leu-Ser-Val-Ile-Met-Glu-Glu (SEQ ID NO: 2, 1-228).

18. The novel collectin according to any one of claims 13 to 17, which is derived from human.

19. The novel collectin consisting of the amino acid sequence that comprises deletion, substitution and/or addition of one or more amino acids in the collectin according to any one of claims 13 to 18, and said novel collectin comprises (1) Ca^{2+}-dependent carbohydrate recognition domain (CRD), and (2) collagen-like region.

20. A vector which comprises the polynucleotide according to any one of the claims 1 to 12 in a manner that allows expression of the novel collectin.

21. A host cell comprising the vector according to claim 20 in a manner that allows the expression.

22. A probe for screening the novel collectin related molecular species comprising the polynucleotide according to any one of claims 1 to 12 or a fragment thereof.

23. An antibody having specific immunoreactivity with the novel collectin according to any one of claims 13 to 19.

24. The antibody according to claim 23, which is a monoclonal antibody.

25. The antibody according to claim 23 or 24 having reduced immunogenicity to human.

26. A method for obtaining a novel collectin related molecular species, comprising screening a protein using the antibody according to any one of claims 23 to 25.

27. A method for obtaining a novel collectin and/or derived molecules, comprising screening a protein using the antibody according to any one of claims 23 to 25.

28. The method according to claim 26 or 27, wherein said screening is expression screening of cDNA library.

29. A method of quantitative determination of a novel collectin and/or derived molecules, comprising measuring an amount of the novel collectin and/or derived molecules contained in a test sample using the antibody according to any one of claims 23 to 25.

30. The method according to claim 29, wherein said antibody is employed in ELISA method.

31. A kit for quantitative determination of a novel collectin and/or derived molecules, comprising the antibody according to any one of claims 23 to 25, wherein an amount of the novel collectin and/or derived molecules in a test sample is measured by ELISA method using the antibody.

32. A method for obtaining a novel collectin and/or derived molecules, comprising isolating a novel collectin and/or derived molecules using the antibody according to any one of claims 23 to 25.

33. The method according to claim 32, wherein affinity chromatography by a support bound with said antibody, and/or immunoprecipitation is utilized.

34. The method according to claim 32 or 33, comprising expressing the novel collectin from the polynucleotide according to any one of claims 1 to 12 prior to the isolation step.

35. A transgenic non-human animal that is stably introduced with a recombinant gene comprising the polynucleotide according to any one of claims 1 to 12 into the chromosome, and that can express a novel collectin.

36. A transgenic non-human animal wherein introduction of a gene is effected in a non-human animal comprising a homologue of the novel collectin according to any one of claims 13 to 19, in a manner to modify the gene expression of said homologue.

37. A knockout non-human animal that is obtained by altering a gene encoding a homologue of the novel collectin according to any one of claims 13 to 19 in a non-human animal comprising said homologue, in a manner to inhibit the expression of said homologue.